AMENDMENT TO THE SPECIFICATION:

Please amend the paragraph beginning on page 26, line 5 as follows:

A *Pichia pastoris* sequence was found in the GenBank under Accession No. E12456 (SEQ ID NO: 2) and was described in Japanese Patent Application No. 07145005, incorporated herein by reference. This sequence shows all typical features of an α-1,6-mannosyltransferase and is most homologous to the *S. cerevisiae* OCH1, thus referred to herein as the *Pichia pastoris* OCH1 gene. The nucleotide sequence of this *Pichia pastoris* OCH1 gene is set forth in SEQ ID NO: 2, and the amino acid sequence of the encoded protein is set forth in SEQ ID NO: 3.

Please amend the paragraph beginning on page 26, line 25 as follows:

pGlycoSwitch M5 (5485 bp, SEQ ID NO: 9, graphically depicted in **Figure 3B**) was constructed as follows. An *Xba* I / *Cla* I fragment of pPIC9 (Invitrogen, Carlsbad, CA), containing the *Pichia pastoris* HIS4 transcriptional terminator sequence, was inserted between the *Hind* III and *Eco*R I sites of pGlycoSwitch M8. Afterwards the 2.3 kb *Bgl* II / *Not* I fragment of pGAPZMFManHDEL (Callewaert et al., *FEBS Lett*, 503(2-3):173-178, 2001) containing the GAP promoter and preMFmannosidaseHDEL cassette, was inserted between the *Hind* III and *Not* I sites. The nucleotide sequence of the preMFmannosidaseHDEL cassette is set forth in SEQ ID NO: 8. All restriction sites used for this construction (except for the *Not* I site) were filled in with Klenow DNA polymerase. The unique *Bst*B I site in pGAPZMFmanHDEL was previously eliminated by filling and religation after digestion.